

Fig. 1

Fig.

Fig. 2

ICTB : 471 TGTCA GTGTCTACGG CCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT 530
 || | ||||| || || | ||||| || || | ||||| || || | ||||| || || | |||||
 SLR : 483 GGTGGGAGTTACGGTCTCGGACAACAGGTGGACGGGTAGAACAGTTAGCCACTTGGAA 542

ICTB : 531 GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA 590
 || | ||||| || | | ||||| || || | ||||| || || | ||||| || || | |||||
 SLR : 543 TGACCCCACTCTACCTTGCCCCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA 602

ICTB : 591 CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCCTTTT-CTGCAGCAGCGATCGGGGTGT 649
 || ||||| ||||| ||||| || || | ||||| || || | ||||| || || | |||||
 SLR : 603 TCTCTTGGCGGCTTACCTGTGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT 661

ICTB : 650 GCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGGACGCTTATGT 708
 |||| | |||| ||||| ||||| || || | ||||| || || | ||||| || || | |||||
 SLR : 662 GCGGACGGTGGTGCCCCAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT 720

ICTB : 709 CTGATCCTCACCTACAGTCGCGGTGGCTGGGTTTGTGCGCCATGATTTTGTCTGG 768
 || | | ||||| || || || ||||| || || ||||| || || ||||| || || |||||
 SLR : 721 CTCCTTTTACCAGAGCCGGGGCGGTTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC 780

ICTB : 769 GCGTTATTAGGCTCTACTGGTTTCAACCCCGTCTACCCGCACCCCTGGCGACGCTGGCTA 828
 | | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 SLR : 781 CTGGCCCTTTGTTACTTCTGGTGTTACCCCAATTACCCAAATTTTGGCAACGGTGTCT 840

ICTB : 829 TTCCCAGTCGTATTGGGTGACTAGTCGCGGTGCTCTT-GGTGGCGGTGCTTGACT--- 884
 || || | | | || || || ||||| || || ||||| || || ||||| || || |||||
 SLR : 841 TTGCCCCCTGGC---GATCGCC--GTGGCGGTATATATTAGGTGGGGAGCGTTGATTGCG 894

ICTB : 885 -TG-AGCCGTTGCGCGTGCGCGGTGTTGAGCATCTTTGTGGGGCGTGAAGACAGACGACAAC 942
 || | ||||| || | | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 SLR : 895 GTGGAACCGATTTCGACTCAGGGCCATGAGCATTTTGTGCTGGGGCGGAAGACAGACAGTAAT 954

Fig. 2
(Continued)

+++W++L F + PQ+WG S LHRL G ++W +S L EALG L+A+++ +APF
 SLR : 5 ISIWRSLMFGGSPQEWGRGSLHRLVGVGQSWIQASVLNPHFEALGTALVAIIFIAAPF 64

ICTB : 61 VPSSALGLGLAAIAAYWALLSLTDIDLQATPIHVLVLYWGVDAATGLSPVRAAALVG 120
 ++ LG+ + A+WALL+ D + TPIH LV YW + A+A G SPV+ AA G

SLR : 65 TSTTMLGIFMLLCCAFWALLTFADQPGKGLTPIHVLVFFAYWCISAIAGVGFSPVKMAAASG 124

ICTB : 121 LAKLTLYLLVFALAAARVLNRPRLRSLLSFVVVITSLFVSUYGLNQWYGVVEELATWVDRN 180
 LAKLT L +F LAAR+L+N + + L +VV++ L V YGL Q + GVE+LATW D

SLR : 125 LAKLTANLCLFLLAARLLQNKQWLNRVTVVLLVGLLVGSYGLRQQQVDGVEQLATWNDPT 184

ICTB : 181 SVADFTSRVYSYGLNPNLLAAYLVPTAFSAAAIGVWRGHLPKLLAIAATGASSLCLILT 240
 S +RVYS+LGPNPLLAAYLVP T S +A+ VWR W PKLL + LCL T

SLR : 185 STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVWRRWPKLLGATMVIIVNLLCLFFT 244

ICTB : 241 YSRGGWLG FVAMIFVWALLGLYWFQPRLPAPWRRNLFPVVLGGLVAVLLVAVLGLLEPLRV 300
 SRGGWL +A+ + L +W+ P+LP W+RW P+ + V + A++ +EP+R+

SLR : 245 QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQRNSLPLAIAVAVILGGGALIAVEPIRL 304

ICTB : 301 RVLSIFVGREDSNNFRINVWLAVLQMIQDRPWLIGIGPGNTAFNLVPLYQQARFTALSA 360
 R +SIF GREDSNNFRINW V MI+ RP +GIGPGN AFN +YP Y + RFTALSA

SLR : 305 RAMSIFAGREDSNNFRINWEGVKAMIRARPIIGIGPGNEAFNQIYPYMRPRFTALSA 364

ICTB : 361 YSVPLEVAVEGGLGLTAFAWLLLVTAVTAVRQVSRLLRRDRNPQAFWLMASLAGLMLG 420
 YS+ LE+ VE G+G T WLL VT V V R R+ P+ W+M +LA + G+L

SLR : 365 YSIYLBILVETGVVGFTCMLNLLAVTLGKGVVELVKRCRQTLAPEGIWMGALAAIIGLLV 424

ICTB : 421 HGLFDTVLVYRPEASTLWNLWCIGAIASFQOPSPKQLPPEAEHSDEKM 467
 HG+ DTV YRP STLWNL + +AS W ++ + B+ D+ +

SLR : 425 HGMVDTVWYRPPVSTLWLLVAIVASQWASQAARLEASKEENEDKPL 471

Fig. 3

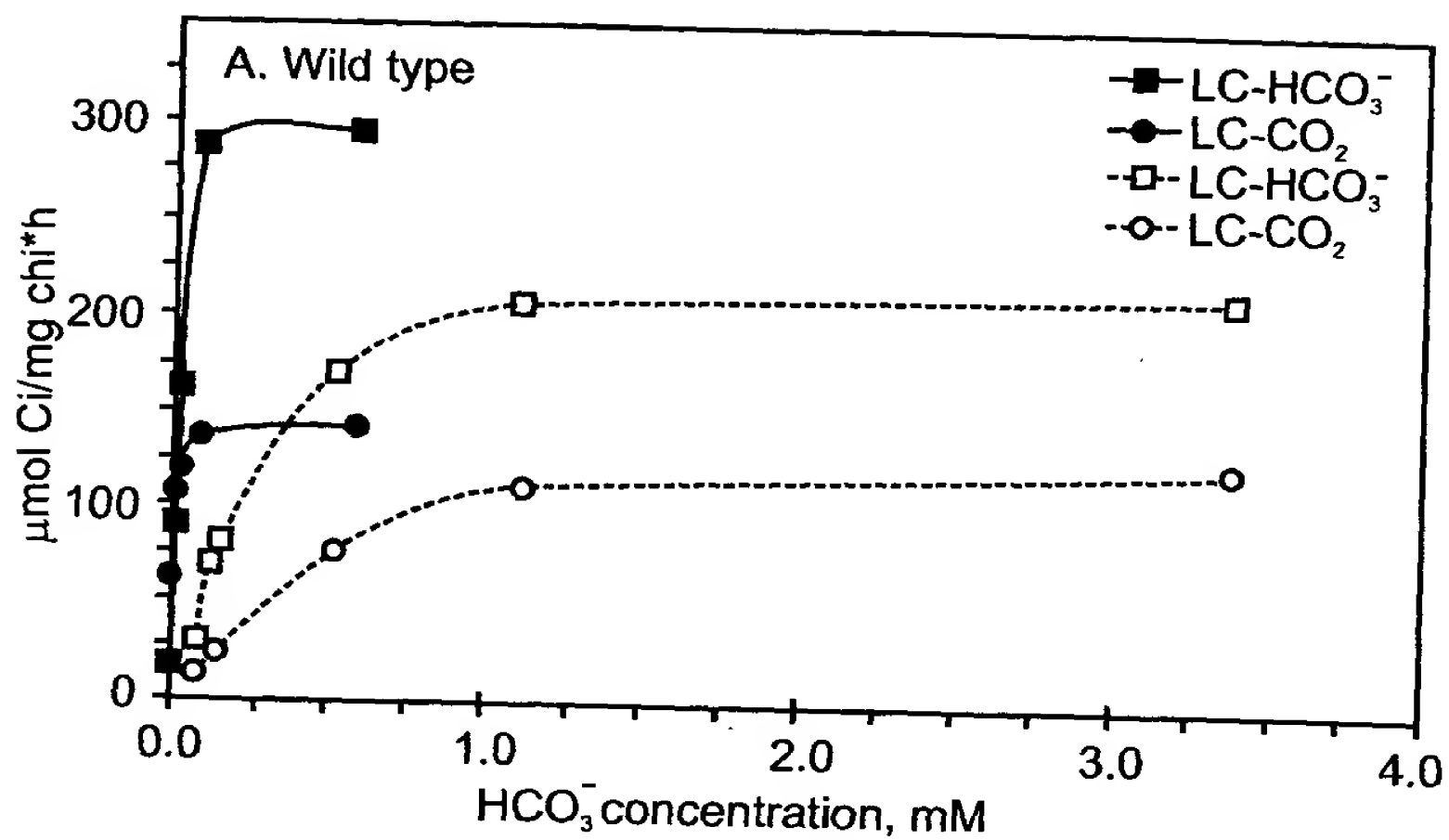


Fig. 4a

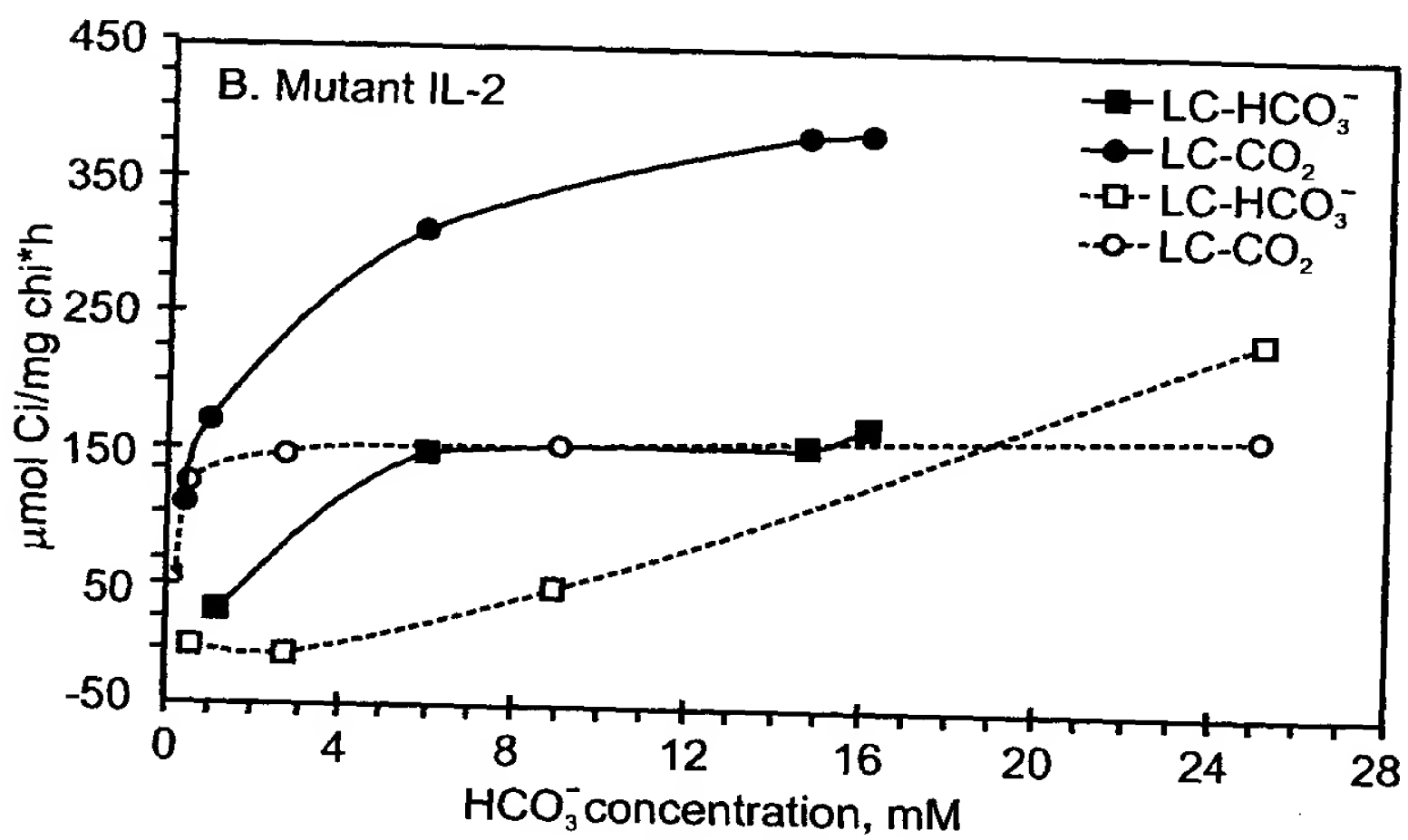


Fig. 4b

Wild type	GGGCT-AGCCCGCGATCGCGGCGCTATTGGGCCC	(SEQ ID NO: 6)
IL-2 ApaI side	GGGCT-AG--G-GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 7)
IL-2 BamHI side	GGGCTCA-----GATCGC-GCCTATTGGGCCC	(SEQ ID NO: 8)
IctB	G L A A I A A Y W A L	(SEQ ID NO: 9)

Fig. 5

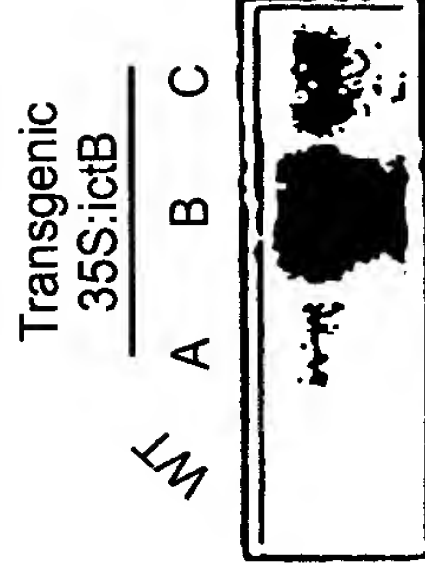


Fig. 6